Sequence search history: STN REGISTRY & HCAPLUS

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=> d stat query L13
L1             1 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLXQSX/SQSP
L2             1 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLXQSX^/SQSP
L3             0 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLFQSM/SQSP
L4             0 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLFQSK/SQSP
L5             0 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLFQSY/SQSP
L6             0 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLYQSM/SQSP
L7             0 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLYQSK/SQSP
L8             0 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDKLYQSY/SQSP
L9             1 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L1 OR L2 OR L3 OR L4
                 OR L5 OR L6 OR L7 OR L8)
L10            1 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L9 AND (("PROTEIN G"
                 OR (PROTEIN(W)G) OR "STREPTOCOCCAL PROTEIN G" OR "STREPTOCOCCUS
                  PROTEIN G") OR ((STREPTOCOCC? OR AUREUS?)(5A)("PROTEIN G" OR
                 PROTEIN(W)G)))
L11            0 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L9 AND (("IGG" OR "IG
                 G" OR "IG-G" OR IG(W)G OR "IMMUNOGLOBULIN G" OR IMMUNOGLOBULIN(
                 W)G OR (IMMUNOGLOBULIN?(3W)("TYPE G" OR TYPE(W)G))))
L12            0 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L9 AND ("IGG BIND" OR
                 "IGG BOUND" OR (("IGG" OR IMMUNOGLOBULIN?)(3A)(BIND? OR BOUND?
                 OR CONJUGAT? OR LIGAND? OR RECOGNI?)))
L13            1 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L9 OR L10 OR L11 OR
                 L12)


=> d stat query L37
L30           44 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDHVAHAY/SQSP
L31            4 SEA FILE=REGISTRY SPE=ON  ABB=ON  PLU=ON  EEDHVAHAY^/SQSP
L32           40 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L30
L33            6 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L31
L34            1 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L32 OR L33) AND
                 (("PROTEIN G" OR (PROTEIN(W)G) OR "STREPTOCOCCAL PROTEIN G" OR
                 "STREPTOCOCCUS PROTEIN G") OR ((STREPTOCOCC? OR AUREUS?)(5A)("P
                 ROTEIN G" OR PROTEIN(W)G)))
L35            1 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L32 OR L33) AND
                 (("IGG" OR "IGG" OR "IG-G" OR IG(W)G OR "IMMUNOGLOBULIN G" OR
                 IMMUNOGLOBULIN(W)G OR (IMMUNOGLOBULIN?(3W)("TYPE G" OR
                 TYPE(W)G))))
L36            0 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L32 OR L33) AND
                 ("IGG BIND" OR "IGG BOUND" OR (("IGG" OR IMMUNOGLOBULIN?)(3A)(B
                 IND? OR BOUND? OR CONJUGAT? OR LIGAND? OR RECOGNI?)))
L37            2 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L34 OR L35 OR L36)
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Sequence search results: STN REGISTRY & HCAPLUS

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=> set gra off
SET COMMAND COMPLETED

=> d L13 1 ibib ed abs hitrn hitseq hitind

L13  ANSWER 1 OF 1  HCAPLUS  COPYRIGHT 2009 ACS on STN
ACCESSION NUMBER:         2005:158774  HCAPLUS  Full-text
DOCUMENT NUMBER:          142:256745
TITLE:                    Engineered subtilisin variants for affinity
                          purification and prodomain-directed processing of
                          fusion proteins and drug delivery use
INVENTOR(S):              Bryan, Philip N.
PATENT ASSIGNEE(S):       University of Maryland Biotechnology Institute, USA
SOURCE:                   PCT Int. Appl., 66 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
     ----------------    ----   --------    --------------------   --------
     WO 2005017110        A2    20050224    WO 2004-US21049        20040629
     WO 2005017110        A3    20081030
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
             LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI,
             NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY,
             TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM,
             AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK,
             EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE,
             SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
             SN, TD, TG, AP, EA, EP, OA
     AU 2004265613        A2    20050224    AU 2004-265613         20040629
     AU 2004265613        A1    20050224
     CA 2534629           A1    20050224    CA 2004-2534629        20040629
     EP 1651751           A2    20060503    EP 2004-777325         20040629
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR
     JP 2007517492        T     20070705    JP 2006-522560         20040629
     CN 101454452         A     20090610    CN 2004-80025223       20060302
     US 20060134740       A1    20060622    US 2006-567073         20060307
PRIORITY APPLN. INFO.:                      US 2003-493032P     P  20030806
                                            WO 2004-US21049     W  20040629

ED   Entered STN:  24 Feb 2005
AB   The present invention is directed to the identification of a protease
     prodomain that is capable of binding a corresponding protease with high
     affinity.  The protease prodomain of the present invention is fused to a
     second protein to form a protease prodomain fusion protein.  The presence of a
     protease prodomain protein in a fusion protein allows for easy and selective
     purification of the second protein by incubation with the corresponding
     protease.  More specifically, mutations to decrease subtilisin BPN' activity
     against non-cognate sequences were introduced. The engineered processing
     subtilisins were immobilized for affinity purification and processing of
```

fusion proteins. The subtilisins of the invention can be used in drug delivery systems.

IT 845921-01-9P
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(engineered subtilisin prodomain containing; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)

IT 845921-01-9P
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(engineered subtilisin prodomain containing; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)

RN 845921-01-9 HCAPLUS
CN Peptide, (Glu-Glu-Asp-Lys-Leu-Xaa-Gln-Ser-Xaa) (9CI) (CA INDEX NAME)

SEQ 1 EEDKLXQSX

IC ICM C12N
CC 7-5 (Enzymes)
Section cross-reference(s): 3, 9, 63

IT Proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(G, fusion products, with subtilisin prodomain; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)

IT 845733-74-6P 845921-01-9P
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(engineered subtilisin prodomain containing; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)

OS.CITING REF COUNT: 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

=> d L37 1-2 ibib ed abs hitrn hitseq hitind

L37 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2009 ACS on STN
ACCESSION NUMBER: 2005:158774 HCAPLUS <<LOGINID::20090811>>
DOCUMENT NUMBER: 142:256745
TITLE: Engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use
INVENTOR(S): Bryan, Philip N.
PATENT ASSIGNEE(S): University of Maryland Biotechnology Institute, USA
SOURCE: PCT Int. Appl., 66 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005017110	A2	20050224	WO 2004-US21049	20040629
WO 2005017110	A3	20081030		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, AP, EA, EP, OA				
AU 2004265613	A2	20050224	AU 2004-265613	20040629
AU 2004265613	A1	20050224		
CA 2534629	A1	20050224	CA 2004-2534629	20040629
EP 1651751	A2	20060503	EP 2004-777325	20040629
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
JP 2007517492	T	20070705	JP 2006-522560	20040629
CN 101454452	A	20090610	CN 2004-80025223	20060302
US 20060134740	A1	20060622	US 2006-567073	20060307

PRIORITY APPLN. INFO.: US 2003-493032P P 20030806
WO 2004-US21049 W 20040629

ED Entered STN: 24 Feb 2005

AB The present invention is directed to the identification of a protease prodomain that is capable of binding a corresponding protease with high affinity. The protease prodomain of the present invention is fused to a second protein to form a protease prodomain fusion protein. The presence of a protease prodomain protein in a fusion protein allows for easy and selective purification of the second protein by incubation with the corresponding protease. More specifically, mutations to decrease subtilisin BPN' activity against non-cognate sequences were introduced. The engineered processing subtilisins were immobilized for affinity purification and processing of fusion proteins. The subtilisins of the invention can be used in drug delivery systems.

IT 845842-00-4DP, variants are claimed
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)

IT 845842-00-4DP, variants are claimed
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)

RN 845842-00-4 HCAPLUS
CN Subtilisin (Bacillus amyloliquefaciens isoenzyme BPN') (9CI) (CA INDEX NAME)

SEQ 1 AGKSNGEKKY IVGFKQTMST MSAAKKKDVI SEKGGKVQKQ FKYVDAASAT
51 LNEKAVKELK KDPSVAYVEE DHVAHAY

IC ICM C12N
CC 7-5 (Enzymes)
Section cross-reference(s): 3, 9, 63
IT Proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(G, fusion products, with subtilisin prodomain; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)
IT 845842-00-4DP, variants are claimed 845842-01-5P
845842-02-6P 845842-03-7P 845842-04-8P 845842-05-9P 845842-06-0P
845842-07-1P 845842-08-2P 845842-09-3P 845842-10-6P 845842-11-7P
845842-12-8P 845842-13-9P 845842-14-0P
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use)
OS.CITING REF COUNT: 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L37 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2009 ACS on STN
ACCESSION NUMBER: 2002:391990 HCAPLUS <<LOGINID::20090811>>
DOCUMENT NUMBER: 136:400590
TITLE: Engineered proteins comprising mutated T cell epitopes for producing hyper- and hypo-allergenic response
INVENTOR(S): Estell, David A.; Harding, Fiona A.
PATENT ASSIGNEE(S): Genencor International, Inc., USA
SOURCE: PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002040997	A2	20020523	WO 2001-US30062	20010926
WO 2002040997	A9	20020725		
WO 2002040997	A3	20040812		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 6936249	B1	20050830	US 2000-677822		20001002
US 6897049	B1	20050524	US 2001-768080		20010123
CA 2424720	A1	20020523	CA 2001-2424720		20010926
AU 2002037646	A	20020527	AU 2002-37646		20010926
JP 2004528013	T	20040916	JP 2002-542874		20010926
PRIORITY APPLN. INFO.:			US 2000-677822	A	20001002
			US 2001-768080	A	20010123
			US 1998-60872	A2	19980415
			US 2000-500135	A2	20000208
			WO 2001-US30062	W	20010926

ED Entered STN: 24 May 2002

AB The present invention relates to a novel methods and compns. for producing hyper and hypo allergenic compns. Specifically, the present invention comprises neutralizing or reducing the ability of T-cells to recognize epitopes and thus prevent sensitization of an individual to the protein. Alternatively, T-cell epitopes are mutated to produce increased immunogenic reactions. The invention also provides method for determining allergenic potential of an engineered protein or enzyme (such as protease).

IT 431541-68-3
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; engineered proteins comprising mutated T cell epitopes for producing hyper- and hypo-allergenic response)

IT 431541-68-3
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; engineered proteins comprising mutated T cell epitopes for producing hyper- and hypo-allergenic response)

RN 431541-68-3 HCAPLUS

CN Subtilisin (Bacillus amyloliquefaciens precursor) (9CI) (CA INDEX NAME)

SEQ

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  1 RGKKVWMSLL FALALMFTMA FGSTSSAQAA GKSNGEKKYM VGFKQTMSTM
 51 SAAKKKDVMS EKGGKVQKQF KYVDAASATL NEKAVKELKK DPSVAYVEED
101 HVAHAYAQSV PYGVSQMKAP ALHSQGYTGS NVKVAVIDSG MDSSHPDLKV
151 AGGASMVPSE TNPFQDNNSH GTHVAGTVAA LNNSIGVLGV APSASLYAVK
201 VLGADGSGQY SWMINGMEWA MANNMDVMNM SLGGPSGSAA LKAAVDKAVA
251 SGVVVVAAAG NEGTSGSSST VGYPGKYPSV MAVGAVDSSN QRASFSSVGP
301 ELDVMAPGVS IQSTLPGNKY GAYNGTSMAS PHVAGAAALM LSKHPNWTNT
351 QVRSSLENTT TKLGDSFYYG KGLMNVQAAA Q
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IC ICM G01N033-53

CC 15-2 (Immunochemistry)
Section cross-reference(s): 2, 3, 7, 62, 63

IT Antibodies and Immunoglobulins
RL: ANT (Analyte); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(IgG; engineered proteins comprising mutated T cell epitopes for producing hyper- and hypo-allergenic response)

IT 431541-68-3 431541-69-4, Subtilisin (human precursor)
431541-70-7, Subtilisin (Bacillus subtilis) 431541-71-8, Subtilisin

(Bacillus licheniformis) 431541-72-9, Subtilisin (Bacillus lentus) 431541-74-1, Glucanase, endo- (Humicola insolens) 431541-75-2, Lipase (Thermomyces lanuginosa) 431541-76-3 431541-77-4
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; engineered proteins comprising mutated T cell epitopes for producing hyper- and hypo-allergenic response)

OS.CITING REF COUNT: 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

Inventor search history

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=> d his L23

     (FILE 'HCAPLUS' ENTERED AT 16:23:59 ON 11 AUG 2009)
L23          17 S L20 OR L22

=> d que L23
L15         203 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  BRYAN P?/AU
L16          54 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L15 AND MARYLAND?/CO,C
                S,PA,SO
L18          11 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L15 AND (("IGG" OR
                "IG G" OR "IG-G" OR IG(W)G OR "IMMUNOGLOBULIN G" OR IMMUNOGLOBU
                LIN(W)G OR (IMMUNOGLOBULIN?(3W)("TYPE G" OR TYPE(W)G))))
L19          17 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L15 AND (("PROTEIN G"
                OR (PROTEIN(W)G) OR "STREPTOCOCCAL PROTEIN G" OR "STREPTOCOCCUS
                 PROTEIN G") OR ((STREPTOCOCC? OR AUREUS?)(5A)("PROTEIN G" OR
                PROTEIN(W)G)))
L20          17 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L18 OR L19)
L22          16 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L20 AND L16
L23          17 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L20 OR L22


=> d his L26

     (FILE 'MEDLINE, BIOSIS, EMBASE, DRUGU' ENTERED AT 16:26:54 ON 11 AUG 2009)
L26          45 S L24 AND L25

=> d que L26
L15         203 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  BRYAN P?/AU
L16          54 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L15 AND MARYLAND?/CO,C
                S,PA,SO
L18          11 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L15 AND (("IGG" OR
                "IG G" OR "IG-G" OR IG(W)G OR "IMMUNOGLOBULIN G" OR IMMUNOGLOBU
                LIN(W)G OR (IMMUNOGLOBULIN?(3W)("TYPE G" OR TYPE(W)G))))
L19          17 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  L15 AND (("PROTEIN G"
                OR (PROTEIN(W)G) OR "STREPTOCOCCAL PROTEIN G" OR "STREPTOCOCCUS
                 PROTEIN G") OR ((STREPTOCOCC? OR AUREUS?)(5A)("PROTEIN G" OR
                PROTEIN(W)G)))
L20          17 SEA FILE=HCAPLUS SPE=ON  ABB=ON  PLU=ON  (L18 OR L19)
L24         134 SEA L16
L25          51 SEA L20
L26          45 SEA L24 AND L25


=> dup rem L23 L26
FILE 'HCAPLUS' ENTERED AT 16:31:06 ON 11 AUG 2009
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2009 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'MEDLINE' ENTERED AT 16:31:06 ON 11 AUG 2009

FILE 'BIOSIS' ENTERED AT 16:31:06 ON 11 AUG 2009
Copyright (c) 2009 The Thomson Corporation

FILE 'EMBASE' ENTERED AT 16:31:06 ON 11 AUG 2009
Copyright (c) 2009 Elsevier B.V. All rights reserved.
PROCESSING COMPLETED FOR L23
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PROCESSING COMPLETED FOR L26
L28          21 DUP REM L23 L26 (41 DUPLICATES REMOVED)
                ANSWERS '1-17' FROM FILE HCAPLUS
                ANSWER '18' FROM FILE MEDLINE
                ANSWERS '19-21' FROM FILE BIOSIS
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Inventor search results

=> d L28 1-21 ibib ab

L28 ANSWER 1 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2007:844631 HCAPLUS Full-text
DOCUMENT NUMBER: 147:337926
TITLE: The design and characterization of two proteins with 88% sequence identity but different structure and function
AUTHOR(S): Alexander, Patrick A.; He, Yanan; Chen, Yihong; Orban, John; Bryan, Philip N.
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2007), 104(29), 11963-11968, S11963/1-S11963/3
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To identify a simplified code for conformational switching, we have redesigned two natural proteins to have 88% sequence identity but different tertiary structures: a 3-α helix fold and an α/β fold. We describe the design of these homologous heteromorphic proteins, their structural properties as determined by NMR, their conformational stabilities, and their affinities for their resp. ligands: IgG and serum albumin. Each of these proteins is completely folded at 25°, is monomeric, and retains the native binding activity. The complete binding epitope for both ligands is encoded within each of the proteins. The IgG-binding epitope is functional only in the α/β fold, and the albumin-binding epitope is functional only in the 3-α fold. These results demonstrate that two monomeric folds and two different functions can be encoded with only 12% of the amino acids in a protein (7 of 56). The fact that 49 aa in these proteins are compatible with both folds shows that the essential information determining a fold can be highly concentrated in a few amino acids and that a very limited subset of interactions in the protein can tip the balance from one monomer fold to another. This delicate balance helps explain why protein structure prediction is so challenging. Furthermore, because a few mutations can result in both new conformation and new function, the evolution of new folds driven by natural selection for alternative functions may be much more probable than previously recognized.
OS.CITING REF COUNT: 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)
REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 2 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 2007:751147 HCAPLUS Full-text
DOCUMENT NUMBER: 147:228974
TITLE: An artificially evolved albumin binding module facilitates chemical shift epitope mapping of GA domain interactions with phylogenetically diverse albumins
AUTHOR(S): He, Yanan; Chen, Yihong; Rozak, David A.; Bryan, Philip N.; Orban, John
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Protein Science (2007), 16(7), 1490-1494

CODEN: PRCIEI; ISSN: 0961-8368
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Protein G-related albumin-binding (GA) modules occur on the surface of numerous Gram-pos. bacterial pathogens and their presence may promote bacterial growth and virulence in mammalian hosts. We recently used phage display selection to evolve a GA domain, PSD-1 (phage selected domain-1), which tightly bound phylogenetically diverse albumins. With respect to PSD-1's broad albumin binding specificity, it remained unclear how the evolved binding epitope compared to those of naturally occurring GA domains and whether PSD-1's binding mode was the same for different albumins. We investigate these questions here using chemical shift perturbation measurements of PSD-1 with rabbit serum albumin (RSA) and human serum albumin (HSA) and put the results in the context of previous work on structure and dynamics of GA domains. Combined, these data provide insights into the requirements for broad binding specificity in GA-albumin interactions. Moreover, we note that using the phage-optimized PSD-1 protein significantly diminishes the effects of exchange broadening at the binding interface between GA modules and albumin, presumably through stabilization of a ligand-bound conformation. The employment of artificially evolved domains may be generally useful in NMR structural studies of other protein-protein complexes.
REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 3 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2006:749200 HCAPLUS Full-text
DOCUMENT NUMBER: 145:308886
TITLE: Structure, Dynamics, and Stability Variation in Bacterial Albumin Binding Modules: Implications for Species Specificity
AUTHOR(S): He, Yanan; Rozak, David A.; Sari, Nese; Chen, Yihong; Bryan, Philip; Orban, John
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, Biotechnology Institute, University of Maryland, Rockville, MD, 20850, USA
SOURCE: Biochemistry (2006), 45(33), 10102-10109
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Protein G-related albumin-binding (GA) modules are frequently expressed on the surfaces of bacterial cells. The limited amino acid sequence variation among GA modules results in structural and functional differences with possible implications for bacterial pathogenesis and host specificity. In particular, the streptococcal G148-GA3 and F. magna ALB8-GA albumin-binding domains exhibit a degree of structural and dynamic diversity that may account for their varied affinities for different species of albumin. To explore the impact of GA module polymorphisms on albumin binding and specificity, we recently used offset recombinant PCR to shuffle seven artificially constructed representatives of the GA sequence space and scan the phage-displayed recombinant domains for mutations that supported binding to the phylogenetically distinct human and guinea pig serum albumins (HSA and GPSA) (Rozak et al. (2006) Biochem. 45, 3263-3271). Surprisingly, phage selection revealed an overwhelming preference for a single recombinant domain (PSD-1, phage-selected domain-1) regardless of whether the phages were enriched for their abilities to bind one or both of these albumins. We describe here the NMR-derived structure, dynamics, and stability of unbound PSD-1. Our results demonstrate that increased flexibility is not a requirement for broadened specificity, as had been suggested earlier (Johansson et al. (2002) J. Mol. Biol. 316, 1083-1099), because PSD-1 binds the phylogenetically diverse HSA

and GPSA even more tightly than G148-GA3 but is less flexible. The structural basis for albumin-binding specificity is analyzed in light of these new results.
OS.CITING REF COUNT: 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 4 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 2005:1037131 HCAPLUS Full-text
DOCUMENT NUMBER: 143:417773
TITLE: Solution NMR Structures of IgG Binding Domains with Artificially Evolved High Levels of Sequence Identity but Different Folds
AUTHOR(S): He, Yanan; Yeh, Deok Cheon; Alexander, Patrick; Bryan, Philip N.; Orban, John
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Biochemistry (2005), 44(43), 14055-14061 CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We describe here the solution NMR structures of two IgG binding domains with highly homologous sequences but different three-dimensional structures. The proteins, G311 and A219, are derived from the IgG binding domains of their wild-type counterparts, protein G and protein A, resp. Through a series of site-directed mutations and phage display selections, the sequences of G311 and A219 were designed to converge to a point of high-level sequence identity while keeping their resp. wild-type tertiary folds. Structures of both artificially evolved sequences were determined by NMR spectroscopy. The main chain fold of G311 can be superimposed on the wild-type α/β protein G structure with a backbone rmsd of 1.4 Å, and the A219 structure can be overlaid on the wild-type three-α-helix protein A fold also with a backbone rmsd of 1.4 Å. The structure of G311, in particular, accommodates a large number of mutational changes without undergoing a change in the overall fold of the main chain. The structural differences are maintained despite a high level (59%) of sequence identity. These proteins serve as starting points for further expts. that will probe basic concepts of protein folding and conformational switching.
OS.CITING REF COUNT: 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 5 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 6
ACCESSION NUMBER: 2005:1065632 HCAPLUS Full-text
DOCUMENT NUMBER: 143:434415
TITLE: Directed Evolution of Highly Homologous Proteins with Different Folds by Phage Display: Implications for the Protein Folding Code
AUTHOR(S): Alexander, Patrick A.; Rozak, David A.; Orban, John; Bryan, Philip N.
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Biochemistry (2005), 44(43), 14045-14054 CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To better understand how amino acid sequences specify unique tertiary folds, we have used random mutagenesis and phage display selection to evolve proteins with a high degree of sequence identity but different tertiary structures (homologous heteromorphs). The starting proteins in this evolutionary process were the IgG binding domains of streptococcal protein G (GB) and staphylococcal protein A (AB). These nonhomologous domains are similar in size and function but have different folds. GB has an α/β fold, and AB is a three-helix bundle (3-α). IgG binding function is used to select for mutant proteins which retain the correct tertiary structure as the level of sequence identity is increased. A detailed thermodn. anal. of the folding reactions and binding reactions for a pair of homologous heteromorphs (59% identical) is presented. High-resolution NMR structures of the pair are presented by He et al. [(2005) Biochem. 44, 14055-14061]. Because the homologous but heteromorphic proteins are identical at most positions in their sequence, their essential folding signals must reside in the positions of nonidentity. Further, the thermodn. linkage between folding and binding is used to assess the propensity of one sequence to adopt two unique folds. OS.CITING REF COUNT: 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 6 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 2005:1252414 HCAPLUS Full-text
DOCUMENT NUMBER: 144:65652
TITLE: G148-GA3: A streptococcal virulence module with atypical thermodynamics of folding optimally binds human serum albumin at physiological temperatures
AUTHOR(S): Rozak, David A.; Orban, John; Bryan, Philip N.
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Biochimica et Biophysica Acta, Proteins and Proteomics (2005), 1753(2), 226-233
CODEN: BBAPBW; ISSN: 1570-9639
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The third albumin binding domain of streptococcal protein G strain 148 (G148-GA3) belongs to a novel class of prokaryotic albumin binding modules that is thought to support virulence in several bacterial species. Here, we characterize G148-GA3 folding and albumin binding by using differential scanning calorimetry and isothermal titration calorimetry to obtain the most complete set of thermodn. state functions for any member of this medically significant module. When buffered at pH 7.0 the 46-amino acid alpha-helical domain melts at 72 °C and exhibits marginal stability (15 kJ/mol) at 37 °C. G148-GA3 unfolding is characterized by small contributions to entropy from non-hydrophobic forces and a low ΔCp (1.1 kJ/(deg mol)). Isothermal titration calorimetry reveals that the domain has evolved to optimally bind human serum albumin near 37 °C with a binding constant of 1.4 + 107 M-1. Anal. of G148-GA3 thermodn. suggests that the domain experiences atypically small per residue changes in structural dynamics and heat capacity while transiting between folded and unfolded states. OS.CITING REF COUNT: 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 7 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 8
ACCESSION NUMBER: 2000:22096 HCAPLUS Full-text
DOCUMENT NUMBER: 132:177168
TITLE: Structure and Dynamics of an Acid-Denatured

Protein G Mutant
AUTHOR(S): Sari, Nese; Alexander, Patrick; Bryan, Philip N.; Orban, John
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Biochemistry (2000), 39(5), 965-977
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB NMR studies of protein denatured states provide insights into potential initiation sites for folding that may be too transient to be observed kinetically. We have characterized the structure and dynamics of the acid-denatured state of protein G by using a F30H mutant of GB1 which is on the margin of stability. At 5 °C, F30H-GB1 is greater than 95% folded at pH 7.0 and is greater than 95% unfolded at pH 4.0. This range of stability is useful because the denatured state can be examined under relatively mild conditions which are optimal for folding GB1. We have assigned almost all backbone 15N, HN, and Hα resonances in the acid-denatured state. Chemical shift, coupling constant, and NOE data indicate that the denatured state has considerably more residual structure when studied under these mild conditions than in the presence of chemical denaturants. The acid-denatured state populates nativelike conformations with both α-helical and β-hairpin characteristics. To our knowledge, this is the first example of a denatured state with NOE and coupling constant evidence for β-hairpin character. A number of non-native turn structures are also detected, particularly in the region corresponding to the β1-β2 hairpin of the folded state. Steady-state {1H-15N} NOE results demonstrate restricted backbone flexibility in more structured regions of the denatured protein. Overall, our studies suggest that regions of the helix, the β3-β4 hairpin, and the β1-β2 turn may serve as potential initiation sites for folding of GB. Furthermore, residual structure in acid-denatured F30H-GB1 is more extensive than in peptide fragments corresponding to the β1-β2, α-helix, and β3-β4 regions, suggesting addnl. medium-to-long-range interactions in the full-length polypeptide chain. OS.CITING REF COUNT: 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)
REFERENCE COUNT: 87 THERE ARE 87 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 8 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 9
ACCESSION NUMBER: 1997:169220 HCAPLUS Full-text
DOCUMENT NUMBER: 126:247958
ORIGINAL REFERENCE NO.: 126:47871a,47874a
TITLE: pKa Measurements from Nuclear Magnetic Resonance for the B1 and B2 Immunoglobulin G -Binding Domains of Protein G: Comparison with Calculated Values for Nuclear Magnetic Resonance and X-ray Structures
AUTHOR(S): Khare, Devesh; Alexander, Patrick; Antosiewicz, Jan; Bryan, Philip; Gilson, Michael; Orban, John
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Biochemistry (1997), 36(12), 3580-3589
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Two-dimensional homo- and heteronuclear NMR (NMR) spectroscopy was used to determine pKa values for all of the acidic residues in the B1 and B2 IgG-(IgG)

binding domains of protein G . Due to the stability of protein G over a wide pH range, ests. of ionization consts. were also obtained for some basic residues. These exptl. determined ionization consts. were compared with values calculated from both X-ray and NMR-derived structures of B1 and B2 using the UHBD algorithm [Antosiewicz, J., et al. (1994) J. Mol. Biol. 238, 415-436]. This algorithm has been found to be predictive for pKa measurements in proteins and, in combination with exptl. measurements, allowed some evaluation of the NMR and X-ray structures. Three regions where significant differences exist between the X-ray and NMR structures are (1) the position of the E56 side chain relative to the backbone amides of K10 and D40, (2) residues 33-37 in the helix, and (3) the Y45 side-chain conformation. For all three cases, the exptl. pH titration curves are notably more consistent with the X-ray structures than the NMR structures. In contrast, a number of solvent-accessible side chains have exptl. pKas more in agreement with mean pKas calculated from families of NMR structures. The conformations of these side chains may be susceptible to crystal packing effects. From titration expts. under basic conditions, it is noteworthy that the chemical shift of the Y45 CεH resonance is invariant up to pDcorr 12. The Y45 side-chain hydroxyl group appears to maintain a nativelike hydrogen bond with D47 at pDcorr 12, even though the protein is approx. 90% unfolded. These results suggest that this short-range (i, i + 2) interaction, located in the β3-β4 hairpin, is present in the high-pH denatured state and may therefore form early in the folding of protein G. OS.CITING REF COUNT: 37 THERE ARE 37 CAPLUS RECORDS THAT CITE THIS RECORD (37 CITINGS)
REFERENCE COUNT: 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 9 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 10
ACCESSION NUMBER: 1995:897077 HCAPLUS Full-text
DOCUMENT NUMBER: 123:308997
ORIGINAL REFERENCE NO.: 123:55219a,55222a
TITLE: Assessment of Stability Differences in the Protein G B1 and B2 Domains From Hydrogen-Deuterium Exchange: Comparison with Calorimetric Data
AUTHOR(S): Orban, John; Alexander, Patrick; Bryan, Philip ; Khare, Devesh
CORPORATE SOURCE: Biotechnology Institute, University of Maryland, Rockville, MD, 20850, USA
SOURCE: Biochemistry (1995), 34(46), 15291-300 CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Hydrogen-deuterium (H-D) exchange expts. have been used to measure exchange rates for almost all of the main-chain amide protons (NHs) in the B1 and B2 IgG-binding domains of protein G. For H-bonded NHs, exchange rates were also measured as a function of temperature from 25 to 65 °C for B1 and from 25 to 60 °C for B2. A number of NHs exchange by a mechanism consistent with global unfolding. For these residues, the free energy required for transient opening of a H-bonded NH (ΔGop) from H-D exchange approximates the extrapolated free energy of thermal unfolding (ΔGu) from calorimetry in B1 and B2. The difference in exchange rates between B1 and B2 for these residues reflects the 1 kcal mol-1 difference in stability from calorimetry. The more stable B1 domain appears to have a slightly larger core of residues which exchange by global unfolding than B2. The ΔGop values for slow exchange H-bonded NHs and calorimetric ΔGu provide highly complementary information on the ΔG vs. temperature stability profiles of B1 and B2. Furthermore, NH exchange rates provide a very sensitive measure of local stability differences between B1 and B2. In both domains, the β2-strand is the least stable of the β-sheet although it is more stable in B1 than B2. The largest

local stability differences occur at residues Y3 and T18 which exchange 40-fold and 100-fold slower in B1, resp. These residues form a H-bond donor-acceptor pair at one end of the β1–β2 hairpin region. Local stability differences are also evident near the β1–β2 turn. These stability differences are, at least in part, due to subtle differences in hydrophobic packing effects. They are not obvious from inspection of the B1 and B2 structures but are manifested as readily measurable changes in NH exchange rates for individual residues. Knowledge of these local stability differences in the β1–β2 region provides potential approaches for designing new stability mutants in protein G. Most non-H-bonded NHs have exchange rates that are <15 times slower than their intrinsic rates. In marked contrast, the NHs of K10, T11, and L12 in the β1–β2 turn and V21 have exchange rates which are five to ≥24 times faster than their intrinsic rates, probably due to local electrostatic effects. For some slow exchanging NHs, particularly in the β3–β4 hairpin region, the ΔGop value is greater than ΔGu by up to 1 kcal mol-1, suggesting that some residual structure may exist in the unfolded state. OS.CITING REF COUNT: 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)

L28 ANSWER 10 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 11
ACCESSION NUMBER: 1994:403496 HCAPLUS Full-text
DOCUMENT NUMBER: 121:3496
ORIGINAL REFERENCE NO.: 121:779a,782a
TITLE: Hydrogen-Deuterium Exchange in the Free and Immunoglobulin G-Bound Protein G B-Domain
AUTHOR(S): Orban, John; Alexander, Patrick; Bryan, Philip
CORPORATE SOURCE: Biotechnology Institute, University of Maryland, Rockville, MD, 20850, USA
SOURCE: Biochemistry (1994), 33(19), 5702-10
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Hydrogen-deuterium exchange expts. have been used to measure backbone amide proton (NH) exchange rates in the free and IgG-bound protein G B2-domain (GB2). Exchange rates were analyzed in terms of the free energy required for transient opening of an H-bonded NH (ΔGop), and exchange mechanisms were interpreted in the context of local and global opening motions. In free GB2 at 22 °C, 28 detectable NHs have ΔGop values which approx. the free energy of thermal unfolding (ΔGu) obtained from calorimetry. This indicates that the majority of detectable NHs exchange through a global unfolding mechanism, reflecting the cooperative two-state unfolding behavior observed thermodynamically [Alexander et al. (1992) Biochem. 31, 3597-3603]. IgG binding results in a broadening of exchange rates and ΔGop values, consistent with a less cooperative exchange mechanism than in free GB2. The large range of protection factors (1.3 to >210) also indicates that exchange does not occur cooperatively for all detectable NHs in bound GB2. Nineteen of the detectable NHs have significantly slowed exchange rates in the complex with protection factors >5. Residues with protection factors of the order of 100 or more occur in both the helix region (F30, K31, A34) and in the central core of the β-sheet (V6, F52, V54). The highest protection factors are consistent with a binding constant of .apprx.108 M-1. The pattern of high protection observed in the helix overlaps with the putative binding site suggested from previous studies. However, the highly protected residues in the central core of the β-sheet are removed from the putative binding interface. This suggests that IgG binding affects conformational dynamics in GB2. The highly protected residues, which are mostly buried from the solvent-accessible surface, constitute the slow-exchange core of bound GB2 and most likely exchange as a cooperative unit by global unfolding. Thus, the rigid slow-exchange core, probably corresponds with the folding core of the bound protein. Residues with intermediate protection factors

are situated further out from the slow-exchange core and the smallest protection factor residues are near the surface or at the ends of β-strands. These latter residues can exchange in the complex without complete unfolding of bound GB2. While these locally unfolded states are still energetically costly, they do not greatly disrupt IgG binding. However, globally unfolded states are not consistent with binding to IgG. OS.CITING REF COUNT: 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS

RECORD (27 CITINGS)

L28 ANSWER 11 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 12
ACCESSION NUMBER: 1994:267651 HCAPLUS Full-text
DOCUMENT NUMBER: 120:267651
ORIGINAL REFERENCE NO.: 120:47363a,47366a
TITLE: Two Crystal Structures of the B1 Immunoglobulin-Binding Domain of Streptococcal Protein G and Comparison with NMR
AUTHOR(S): Gallagher, Travis; Alexander, Patrick; Bryan, Philip; Gilliland, Gary L.
CORPORATE SOURCE: Biotechnology Institute, University of Maryland, Rockville, MD, 20850, USA
SOURCE: Biochemistry (1994), 33(15), 4721-9
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The structure of the 56-residue B1 Ig-binding domain from streptococcal protein G has been determined in two different crystal forms. The crystal structures were deduced by mol. replacement, based on the structure of the B2 domain (Brookhaven accession code 1PGX). Final R values are 0.174 and 0.198 for orthorhombic and trigonal forms, for diffraction data from 6.0 to 2.07 Å and from 6 to 1.92 Å, resp. The orthorhombic crystals have an unusually high packing d. for protein crystals, with Vm = 1.66 and a solvent content of 26%. The protein structure is found to be very similar (rms deviation 0.25 Å for 56 Ca's) in the two crystal forms, with an efficiently packed hydrophobic core between a four-stranded β-sheet and a four-turn α-helix. The B1 domain has the same fold and general structure as the B2 domain (rms deviations 0.36 and 0.39 Å), despite the six residue differences between them. The crystallog. models differ from NMR-derived models in several local regions, primarily in the loop involving residues 46-51; other significant variations are observed in the helix and in the structure of bound water. The primary crystal contact is the same in both crystal forms, involving both sheet edges to form extended β-sheets throughout the crystals.
OS.CITING REF COUNT: 180 THERE ARE 180 CAPLUS RECORDS THAT CITE THIS RECORD (182 CITINGS)

L28 ANSWER 12 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 13
ACCESSION NUMBER: 1992:488248 HCAPLUS Full-text
DOCUMENT NUMBER: 117:88248
ORIGINAL REFERENCE NO.: 117:15367a,15370a
TITLE: Kinetic analysis of folding and unfolding the 56 amino acid IgG-binding domain of streptococcal protein G
AUTHOR(S): Alexander, Patrick; Orban, John; Bryan, Philip
CORPORATE SOURCE: Cent. Adv. Res. Biotechnol., Maryland Biotechnol. Inst., Rockville, MD, 20850, USA
SOURCE: Biochemistry (1992), 31(32), 7243-8
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The 56 amino acid B domain of protein G (GB) is a stable globular folding unit with no disulfide cross-links. The phys. properties of GB offer extraordinary

flexibility for evaluating the energetics of the folding reaction. The protein is monomeric and very soluble in both folded and unfolded forms. The folding reaction has been previously examined by differential scanning calorimetry (Alexander et al., 1992) and found to exhibit 2-state unfolding behavior over a wide pH range with an unfolding transition near 90° (GB1) at neutral pH. Here, the kinetics of folding and unfolding of 2 naturally occurring versions of GB were measured using stopped-flow mixing methods and analyzed according to transition-state theory. GB contains no prolines, and the kinetics of folding and unfolding can be fit to a single, first-order rate constant over the temperature range of 5-35°. The major thermodn. changes going from the unfolded state to the transition state are (1) a large decrease in heat capacity (ΔCp), indicating that the transition state is compact and solvent inaccessible relative to the unfolded state; (2) a large loss of entropy; and (3) a small increase in enthalpy. The most surprising feature of the folding of GB compared to that of previously studied proteins is that its folding approximates a rapid diffusion controlled process with little increase in enthalpy going from the unfolded to the transition state.

OS.CITING REF COUNT: 103 THERE ARE 103 CAPLUS RECORDS THAT CITE THIS RECORD (103 CITINGS)

L28 ANSWER 13 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 14
ACCESSION NUMBER: 1992:168554 HCAPLUS Full-text
DOCUMENT NUMBER: 116:168554
ORIGINAL REFERENCE NO.: 116:28367a,28370a
TITLE: Sequence-specific proton NMR assignments and secondary structure of the streptococcal protein G B2-domain
AUTHOR(S): Orban, John; Alexander, Patrick; Bryan, Philip
CORPORATE SOURCE: Cent. Adv. Res. Biotechnol., Univ. Maryland, Rockville, MD, 20850, USA
SOURCE: Biochemistry (1992), 31(14), 3604-11
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two-dimensional NMR spectroscopy was used to obtain sequence-specific 1H NMR assignments for the IgG-binding B2-domain of streptococcal protein G. Secondary structure elements were identified from anal. of characteristic backbone-backbone NOE patterns and amide proton exchange data. The B2-domain contains a 4-stranded β-sheet region in which the 2 inner strands form a parallel β-sheet with each other and antiparallel β-sheets with the outer strands. The outer strands are connected via a 16-residue α-helix and short loops on both ends of the helix. The α-helix and β-sheet structures contain well-defined polar and apolar sides, and numerous long-range NOEs from the apolar helix to apolar sheet regions were used to derive a model for the global fold of the B2-domain. While the overall fold is similar to that obtained for B1-type domains, differences in amide proton exchange rates and hydrophobic packing are observed

OS.CITING REF COUNT: 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)

L28 ANSWER 14 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 15
ACCESSION NUMBER: 1992:168553 HCAPLUS Full-text
DOCUMENT NUMBER: 116:168553
ORIGINAL REFERENCE NO.: 116:28367a,28370a
TITLE: Thermodynamic analysis of the folding of the streptococcal protein G IgG-binding domains B1 and B2: why small proteins tend to have high denaturation temperatures
AUTHOR(S): Alexander, Patrick; Fahnestock, Stephen; Lee, Timothy; Orban, John; Bryan, Philip
CORPORATE SOURCE: Cent. Adv. Res. Biotechnol., Univ. Maryland,

Rockville, MD, 20850, USA
SOURCE: Biochemistry (1992), 31(14), 3597-603
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two naturally occurring variations of the IgG-binding domain of streptococcal protein G were cloned, expressed, and characterized. The domain is a stable cooperative folding unit of 56 amino acids, which maintains a unique folded structure without disulfide cross-links or tight ligand binding. The thermodn. was studied of the unfolding reaction for the two versions of this domain, designated B1 and B2, which differ by 6 amino acids. They have denaturation temps. of 87.5° and 79.4°, resp. at pH 5.4, as determined by differential scanning calorimetry. Thermodn. state functions for the unfolding reaction (ΔG, ΔH, ΔS, and ΔCp) were determined and reveal several interesting insights into the behavior of very small proteins. First, though the B1 domain has a heat denaturation point close to 90°, it is not unusually stable at physiol. relevant temps. (ΔG = 25 kJ/mol at 37°). This behavior occurs because the stability profile (ΔG vs. temperature) is flat and shallow due to the small ΔS and ΔCp for unfolding.
OS.CITING REF COUNT: 147 THERE ARE 147 CAPLUS RECORDS THAT CITE THIS RECORD (147 CITINGS)

L28 ANSWER 15 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN
ACCESSION NUMBER: 2005:158774 HCAPLUS Full-text
DOCUMENT NUMBER: 142:256745
TITLE: Engineered subtilisin variants for affinity purification and prodomain-directed processing of fusion proteins and drug delivery use
INVENTOR(S): Bryan, Philip N.
PATENT ASSIGNEE(S): University of Maryland Biotechnology Institute, USA
SOURCE: PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005017110	A2	20050224	WO 2004-US21049	20040629
WO 2005017110	A3	20081030		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, AP, EA, EP, OA				
AU 2004265613	A2	20050224	AU 2004-265613	20040629
AU 2004265613	A1	20050224		
CA 2534629	A1	20050224	CA 2004-2534629	20040629
EP 1651751	A2	20060503	EP 2004-777325	20040629
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
JP 2007517492	T	20070705	JP 2006-522560	20040629

CN 101454452	A	20090610	CN 2004-80025223	20060302
US 20060134740	A1	20060622	US 2006-**567073**	20060307
PRIORITY APPLN. INFO.:			US 2003-493032P	P 20030806
			WO 2004-US21049	W 20040629

AB The present invention is directed to the identification of a protease prodomain that is capable of binding a corresponding protease with high affinity. The protease prodomain of the present invention is fused to a second protein to form a protease prodomain fusion protein. The presence of a protease prodomain protein in a fusion protein allows for easy and selective purification of the second protein by incubation with the corresponding protease. More specifically, mutations to decrease subtilisin BPN' activity against non-cognate sequences were introduced. The engineered processing subtilisins were immobilized for affinity purification and processing of fusion proteins. The subtilisins of the invention can be used in drug delivery systems. OS.CITING REF COUNT: 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD
(1 CITINGS)

L28 ANSWER 16 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN

ACCESSION NUMBER:	2004:896822 HCAPLUS Full-text
DOCUMENT NUMBER:	142:70728
TITLE:	Engineering subtilisin into a fluoride-triggered processing protease useful for one-step protein purification
AUTHOR(S):	Ruan, Biao; Fisher, Kathryn E.; Alexander, Patrick A.; Doroshko, Viktoriya; Bryan, Philip N.
CORPORATE SOURCE:	Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE:	Biochemistry (2004), 43(46), 14539-14546 CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER:	American Chemical Society
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB Subtilisin BPN' was engineered into a highly specific, processing protease, and the subtilisin pro-domain was co-engineered into an optimized recognition sequence. This involved 5 steps. First, a robust subtilisin mutant was created, which could tolerate the subsequent mutations needed for high specificity. Second, the substrate-binding pocket was mutated to increase its sequence selectivity. Third, the subtilisin pro-domain was engineered to direct cleavage to the junction of any protein fused to it. Fourth, the active site of subtilisin was engineered to kinetically isolate binding and cleavage reactions. Finally, specific anions were identified to trigger the processing reaction, with F- ions being particularly useful. The ability to isolate the binding and processing steps with a triggering mechanism created a protease with a virtual on-off switch. This allowed column-immobilized processing subtilisin to be used as both the affinity ligand and processing protease for 1-step purification of proteins. Fusion proteins tagged with the engineered pro-domain can be bound to the column and washed free of contaminants. Cleavage can be triggered by the addition of F- to release the pure target protein. The column is then regenerated by stripping off the tightly bound pro-domain at pH 2.1. Ten proteins have been purified to date by this method.

OS.CITING REF COUNT:	19	THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
REFERENCE COUNT:	43	THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 17 OF 21 HCAPLUS COPYRIGHT 2009 ACS on STN

ACCESSION NUMBER:	1998:528554 HCAPLUS Full-text
TITLE:	The folding kinetics and stability of proteins G B1: A hydrogen exchange study.
AUTHOR(S):	Tsai, Amos; Bryan, Philip; Orban, John

CORPORATE SOURCE: NIST/CARB, Rockville, MD, 20850, USA
SOURCE: Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (1998), BTEC-105. American Chemical Society: Washington, D. C.
CODEN: 66KYA2
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB The global stability of a protein is commonly characterized by the free energy of unfolding measured by either CD melting or micro-calorimetry. In this paper, a method for measuring the unfolding energy for individual residues within a mol. will be presented. According to Arrington and Robertson [Biochem. 36, 8686-8691, 1997], it is possible to determine the folding and unfolding rates of individual amides of a protein by carrying out hydrogen exchange expts. in the EX1 and EX2 regimes. In this particular study, the exchange expts. were performed betwen pD 5.5 and 10. 1D HMQC measurements in real time were taken for the slowest exchange amides at low pD, and 2D HSQC measurements in the quench mode were taken for the faster exchange amides at high pD. The folding and unfolding rates for 20 out of a total of 56 amides were obtained for protein G B1. Based on these results, I will show that this method is well suited for probing protein stability as a function of solvent condition and mutation.

L28 ANSWER 18 OF 21 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2008622325 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 18796611
TITLE: NMR structures of two designed proteins with high sequence identity but different fold and function.
AUTHOR: He Yanan; Chen Yihong; Alexander Patrick; Bryan Philip N; Orban John
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, 9600 Gudelsky Drive, Rockville, MD 20850, USA.
CONTRACT NUMBER: GM62154 (United States NIGMS NIH HHS)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2008 Sep 23) Vol. 105, No. 38, pp. 14412-7. Electronic Publication: 2008-09-16.
Journal code: 7505876. E-ISSN: 1091-6490.
Report No.: NLM-PMC2567172.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: PDB-2JWS; PDB-2JWU
ENTRY MONTH: 200810
ENTRY DATE: Entered STN: 25 Sep 2008
Last Updated on STN: 23 Oct 2008
Entered Medline: 22 Oct 2008
AB How protein sequence codes for 3D structure remains a fundamental question in biology. One approach to understanding the folding code is to design a pair of proteins with maximal sequence identity but retaining different folds. Therefore, the nonidentities must be responsible for determining which fold topology prevails and constitute a fold-specific folding code. We recently designed two proteins, G(A)88 and G(B)88, with 88% sequence identity but different folds and functions [Alexander et al. (2007) Proc Natl Acad Sci USA 104:11963-11968]. Here, we describe the detailed 3D structures of these proteins determined in solution by NMR spectroscopy. Despite a large number of mutations taking the sequence identity level from 16 to 88%, G(A)88 and

G(B)88 maintain their distinct wild-type 3-alpha and alpha/beta folds, respectively. To our knowledge, the 3D-structure determination of two monomeric proteins with such high sequence identity but different fold topology is unprecedented. The geometries of the seven nonidentical residues (of 56 total) provide insights into the structural basis for switching between 3-alpha and alpha/beta conformations. Further mutation of a subset of these nonidentities, guided by the G(A)88 and G(B)88 structures, leads to proteins with even higher levels of sequence identity (95%) and different folds. Thus, conformational switching to an alternative monomeric fold of comparable stability can be effected with just a handful of mutations in a small protein. This result has implications for understanding not only the folding code but also the evolution of new folds.

L28 ANSWER 19 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
ACCESSION NUMBER: 1999:185914 BIOSIS Full-text
DOCUMENT NUMBER: PREV199900185914
TITLE: Structural and dynamical analysis of an acid-denatured protein G mutant.
AUTHOR(S): Sari, N. [Reprint author]; Alexander, P. [Reprint author]; Bryan, P. [Reprint author]; Orban, J. [Reprint author]
CORPORATE SOURCE: Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, 20850, USA
SOURCE: Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A109. print.
Meeting Info.: Forty-third Annual Meeting of the Biophysical Society. Baltimore, Maryland, USA. February 13-17, 1999.
CODEN: BIOJAU. ISSN: 0006-3495.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 5 May 1999
Last Updated on STN: 5 May 1999

L28 ANSWER 20 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
ACCESSION NUMBER: 1995:282591 BIOSIS Full-text
DOCUMENT NUMBER: PREV199598296891
TITLE: Solution structure of the streptococcal protein G B2 domain at pH 5.4.
AUTHOR(S): Hancock, Diane K. [Reprint author]; Alexander, Patrick; Bryan, Philip; Orban, John
CORPORATE SOURCE: Natl. Inst. Stand. Technol., Maryland Biotechnol. Inst., Cent. Adv. Res. Biotechnol., 9600 Gudelsky Dr., Rockville, MD 20850, USA
SOURCE: Journal of Cellular Biochemistry Supplement, (1995) Vol. 0, No. 21B, pp. 26.
Meeting Info.: Keystone Symposium on Frontiers of NMR in Molecular Biology-IV. Keystone, Colorado, USA. April 3-9, 1995.
ISSN: 0733-1959.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English

ENTRY DATE: Entered STN: 5 Jul 1995
Last Updated on STN: 5 Jul 1995

L28 ANSWER 21 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
ACCESSION NUMBER: 1993:242203 BIOSIS Full-text
DOCUMENT NUMBER: PREV199344115403
TITLE: Solution structure and IgG binding site of the streptococcal protein G B2 domain.
AUTHOR(S): Orban, John [Reprint author]; Alexander, Patrick [Reprint author]; Bryan, Philip [Reprint author]; Hancock, Diane
CORPORATE SOURCE: Univ. Maryland, Maryland Biotechnol. Inst., 9600 Gudelsky Drive, Rockville, MD 20850, USA
SOURCE: Journal of Cellular Biochemistry Supplement, (1993) Vol. 0, No. 17 PART C, pp. 298.
Meeting Info.: Keystone Symposium on Frontiers of NMR in Molecular Biology III. Taos, New Mexico, USA. March 8-14, 1993.
ISSN: 0733-1959.
DOCUMENT TYPE: Conference; (Meeting)
LANGUAGE: English
ENTRY DATE: Entered STN: 15 May 1993
Last Updated on STN: 15 May 1993

Full search history

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=> d his full

     (FILE 'HOME' ENTERED AT 16:08:50 ON 11 AUG 2009)

     FILE 'REGISTRY' ENTERED AT 16:09:01 ON 11 AUG 2009
L1             1 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLXQSX/SQSP
L2             1 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLXQSX^/SQSP
L3             0 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLFQSM/SQSP
L4             0 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLFQSK/SQSP
L5             0 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLFQSY/SQSP
L6             0 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLYQSM/SQSP
L7             0 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLYQSK/SQSP
L8             0 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLYQSY/SQSP

     FILE 'HCAPLUS' ENTERED AT 16:14:16 ON 11 AUG 2009
L9             1 SEA SPE=ON  ABB=ON  PLU=ON  (L1 OR L2 OR L3 OR L4 OR L5 OR L6
                 OR L7 OR L8)
L10            1 SEA SPE=ON  ABB=ON  PLU=ON  L9 AND (("PROTEIN G" OR (PROTEIN(W)
                 G) OR "STREPTOCOCCAL PROTEIN G" OR "STREPTOCOCCUS PROTEIN G")
                 OR ((STREPTOCOCC? OR AUREUS?)(5A)("PROTEIN G" OR PROTEIN(W)G)))

L11            0 SEA SPE=ON  ABB=ON  PLU=ON  L9 AND (("IGG" OR "IG G" OR "IG-G"
                 OR IG(W)G OR "IMMUNOGLOBULIN G" OR IMMUNOGLOBULIN(W)G OR
                 (IMMUNOGLOBULIN?(3W)("TYPE G" OR TYPE(W)G))))
L12            0 SEA SPE=ON  ABB=ON  PLU=ON  L9 AND ("IGG BIND" OR "IGG BOUND"
                 OR (("IGG" OR IMMUNOGLOBULIN?)(3A)(BIND? OR BOUND? OR CONJUGAT?
                  OR LIGAND? OR RECOGNI?)))
L13            1 SEA SPE=ON  ABB=ON  PLU=ON  (L9 OR L10 OR L11 OR L12)

     FILE 'MEDLINE, BIOSIS, EMBASE, DRUGU' ENTERED AT 16:21:48 ON 11 AUG 2009
L14            0 SEA SPE=ON  ABB=ON  PLU=ON  EEDKLXQSX? OR EEDKLFQSM? OR
                 EEDKLFQSK? OR EEDKLFQSY? OR EEDKLYQSM? OR EEDKLYQSK? OR
                 EEDKLYQSY?

     FILE 'HCAPLUS' ENTERED AT 16:23:59 ON 11 AUG 2009
L15          203 SEA SPE=ON  ABB=ON  PLU=ON  BRYAN P?/AU
L16           54 SEA SPE=ON  ABB=ON  PLU=ON  L15 AND MARYLAND?/CO,CS,PA,SO
L17            0 SEA SPE=ON  ABB=ON  PLU=ON  L15 AND (EEDKLXQSX? OR EEDKLFQSM?
                 OR EEDKLFQSK? OR EEDKLFQSY?  OR EEDKLYQSM? OR EEDKLYQSK? OR
                 EEDKLYQSY?)
L18           11 SEA SPE=ON  ABB=ON  PLU=ON  L15 AND (("IGG" OR "IG G" OR
                 "IG-G" OR IG(W)G OR "IMMUNOGLOBULIN G" OR IMMUNOGLOBULIN(W)G
                 OR (IMMUNOGLOBULIN?(3W)("TYPE G" OR TYPE(W)G))))
L19           17 SEA SPE=ON  ABB=ON  PLU=ON  L15 AND (("PROTEIN G" OR (PROTEIN(W
                 )G) OR "STREPTOCOCCAL PROTEIN G" OR "STREPTOCOCCUS PROTEIN G")
                 OR ((STREPTOCOCC? OR AUREUS?)(5A)("PROTEIN G" OR PROTEIN(W)G)))

L20           17 SEA SPE=ON  ABB=ON  PLU=ON  (L18 OR L19)
L21            0 SEA SPE=ON  ABB=ON  PLU=ON  L15 AND NONAPEPTID?
L22           16 SEA SPE=ON  ABB=ON  PLU=ON  L20 AND L16
L23           17 SEA SPE=ON  ABB=ON  PLU=ON  L20 OR L22

     FILE 'MEDLINE, BIOSIS, EMBASE, DRUGU' ENTERED AT 16:26:54 ON 11 AUG 2009
L24          134 SEA SPE=ON  ABB=ON  PLU=ON  L16
L25           51 SEA SPE=ON  ABB=ON  PLU=ON  L20
L26           45 SEA SPE=ON  ABB=ON  PLU=ON  L24 AND L25
L27            0 SEA SPE=ON  ABB=ON  PLU=ON  L26 AND NONAPEPTID?
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                D STAT QUERY L13
                SET GRA OFF

     FILE 'HCAPLUS' ENTERED AT 16:30:34 ON 11 AUG 2009
                D L13 1 IBIB ED ABS HITRN HITSEQ HITIND

     FILE 'MEDLINE, BIOSIS, EMBASE, DRUGU' ENTERED AT 16:30:35 ON 11 AUG 2009
                D QUE L23
                D QUE L26

     FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE' ENTERED AT 16:31:06 ON 11 AUG 2009
L28           21 DUP REM L23 L26 (41 DUPLICATES REMOVED)
                     ANSWERS '1-17' FROM FILE HCAPLUS
                     ANSWER '18' FROM FILE MEDLINE
                     ANSWERS '19-21' FROM FILE BIOSIS
                D L28 1-21 IBIB AB
                D COST

     FILE 'REGISTRY' ENTERED AT 17:01:37 ON 11 AUG 2009
L29            0 SEA SPE=ON  ABB=ON  PLU=ON  EEDHVAHAY/SQEP
L30           44 SEA SPE=ON  ABB=ON  PLU=ON  EEDHVAHAY/SQSP
L31            4 SEA SPE=ON  ABB=ON  PLU=ON  EEDHVAHAY^/SQSP

     FILE 'HCAPLUS' ENTERED AT 17:02:42 ON 11 AUG 2009
L32           40 SEA SPE=ON  ABB=ON  PLU=ON  L30
L33            6 SEA SPE=ON  ABB=ON  PLU=ON  L31
L34            1 SEA SPE=ON  ABB=ON  PLU=ON  (L32 OR L33) AND (("PROTEIN G" OR
                 (PROTEIN(W)G) OR "STREPTOCOCCAL PROTEIN G" OR "STREPTOCOCCUS
                 PROTEIN G") OR ((STREPTOCOCC? OR AUREUS?)(5A)("PROTEIN G" OR
                 PROTEIN(W)G)))
L35            1 SEA SPE=ON  ABB=ON  PLU=ON  (L32 OR L33) AND (("IGG" OR "IGG"
                 OR "IG-G" OR IG(W)G OR "IMMUNOGLOBULIN G" OR IMMUNOGLOBULIN(W)G
                  OR (IMMUNOGLOBULIN?(3W)("TYPE G" OR TYPE(W)G))))
L36            0 SEA SPE=ON  ABB=ON  PLU=ON  (L32 OR L33) AND ("IGG BIND" OR
                 "IGG BOUND" OR (("IGG" OR IMMUNOGLOBULIN?)(3A)(BIND? OR BOUND?
                 OR CONJUGAT? OR LIGAND? OR RECOGNI?)))
L37            2 SEA SPE=ON  ABB=ON  PLU=ON  (L34 OR L35 OR L36)
                D STAT QUERY L37
                SET GRA OFF
                D L37 1-2 IBIB ED ABS HITRN HITSEQ HITIND


     FILE HOME

     FILE REGISTRY
     Property values tagged with IC are from the ZIC/VINITI data file
     provided by InfoChem.

     STRUCTURE FILE UPDATES:   10 AUG 2009  HIGHEST RN 1173881-48-5
     DICTIONARY FILE UPDATES:  10 AUG 2009  HIGHEST RN 1173881-48-5

     New CAS Information Use Policies, enter HELP USAGETERMS for details.

     TSCA INFORMATION NOW CURRENT THROUGH January 9, 2009.

       Please note that search-term pricing does apply when
       conducting SmartSELECT searches.

     REGISTRY includes numerically searchable data for experimental and
     predicted properties as well as tags indicating availability of
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experimental property data in the original document. For information on property searching in REGISTRY, refer to:

http://www.cas.org/support/stngen/stndoc/properties.html

FILE HCAPLUS

FILE COVERS 1907 - 11 Aug 2009 VOL 151 ISS 7
FILE LAST UPDATED: 10 Aug 2009 (20090810/ED)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Jun 2009
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Jun 2009

HCAplus now includes complete International Patent Classification (IPC) reclassification data for the second quarter of 2009.

CAS Information Use Policies apply and are available at:

http://www.cas.org/legal/infopolicy.html

This file contains CAS Registry Numbers for easy and accurate substance identification.

The ALL, BIB, MAX, and STD display formats in the CA/CAplus family of databases have been updated to include new citing references information. This enhancement may impact record import into database management software. For additional information, refer to NEWS 9.

FILE MEDLINE
FILE LAST UPDATED: 8 Aug 2009 (20090808/UP). FILE COVERS 1949 TO DATE.

MEDLINE and LMEDLINE have been updated with the 2009 Medical Subject Headings (MeSH) vocabulary and tree numbers from the U.S. National Libra of Medicine (NLM). Additional information is available at

http://www.nlm.nih.gov/pubs/techbull/nd08/nd08_medline_data_changes_2009.

On February 21, 2009, MEDLINE was reloaded. See HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

See HELP RANGE before carrying out any RANGE search.

FILE BIOSIS
FILE COVERS 1926 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1926 TO DATE.

RECORDS LAST ADDED: 5 August 2009 (20090805/ED)

BIOSIS has been augmented with 1.8 million archival records from 1926 through 1968. These records have been re-indexed to match current BIOSIS indexing.

FILE EMBASE
FILE COVERS 1974 TO 11 Aug 2009 (20090811/ED)

EMBASE was reloaded on March 30, 2008.

EMBASE is now updated daily. SDI frequency remains weekly (default) and biweekly.

This file contains CAS Registry Numbers for easy and accurate substance identification.

Beginning January 2008, Elsevier will no longer provide EMTREE codes as part of the EMTREE thesaurus in EMBASE. Please update your current-awareness alerts (SDIs) if they contain EMTREE codes.

For further assistance, please contact your local helpdesk.

FILE DRUGU
FILE LAST UPDATED: 4 AUG 2009 <20090804/UP>
>>> DERWENT DRUG FILE (SUBSCRIBER) <<<

>>> FILE COVERS 1983 TO DATE <<<
>>> THESAURUS AVAILABLE IN /CT <<<